

*(The following are the names of the persons who have been elected to the various offices of the Association, as reported by the Secretary.)*

<120> Prostate Cancer-Specific Marker

<140> to be assigned

<150> 60/041,246

<150> 60/047,811

<151> 1997-05-15

<150> 09/036,315

<151> 1998-03-06

<150> 09/535,597

<151> 2000-03-27

<160> 27

&lt;170&gt; PatentIn Ver. 2.1

<210> 1

<211> 3891

<212> DNA

<213> Homo sapiens

**<220>**

<221> CDS

<222> (151) .. (1425)

**<220>**

<223> product = Repro-PC-1.0

**<400> 1**

ctctttgcct cctccctggt ccaggagctg gtgccctggg ctctgcgctg ttgttttcag 60

cgttccgaaa gccggcgctt gagatccagg caagtgaatc cagccaggca gttttccctt 120

cagcacctcg gacagaacac gcagtaaaaa atg gct ccg atc acc acc agc cgg 174  
Met Ala Pro Ile Thr Thr Ser Arg

5

[illegible]



380

385

390

ttg ggt gca gca gca gaa gga act ggt gga gag cac tgg aaa gag atc 1374  
 Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile  
 395 400 405

tgt gac tac ccc agg aga caa att gcc aag tgg cac gtg ctc tgt gat 1422  
 Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp  
 410 415 420

ggt tagcatccta gccgtgagtt ggaacttaaa ggtttttact aggcaaggag 1475  
 Gly  
 425

aaattttctt tctttctata ttggattgca agcttgggaa atcaagctac ctttttggtg 1535

ttgttggtgt tgctagaaat ggattgaatt agtagaccag aaagtaactt caaatgtgta 1595

ttatgataat ttccctatatt attagaagag ttggataaat tttcataaga tattcaatat 1655

ctccttcaga ttaccagtga tataactagg aatagtcaga cattttatga atactgtgcc 1715

agaatcccaa attataaatg tgacaatctc attggaacat gtcacaaaaa gttaatgtga 1775

ttaagattta aaaacgaaaa gtatgccttg ccttggtgaaa atttatccat ttatcttcag 1835

gttgggggaa atcaattttt ctttaattca aagatactaa aaaaatgtcc tccagtttgt 1895

atttattaat tctgtcatgt gcaaattggt gtccctgcata taaaagtatc tggtcatttc 1955

agtttggttt gtaattattt gatgcaattt tatcataaga gtaactcaga ttcatttcaa 2015

aaggacagtg aacaagctga gaaattattt tatcaaaggg ctgagttgag aacactgtgg 2075

ctgaaatata atttttctcc ccctaagggt tacatgtgag tcaaaatttt gtaaaatata 2135

acctcacata agaaccatgg ccttggtatta ttcactgcct gtcacaagcc tcagtgtggc 2195

ctgagaaatc cctatgtacc tttgtgaaat tgttgaatta gttagtgaat aaagaaataa 2255

acttcaacta gaaatccagt tagaagtgca attttcttat aggaaatagg tatagtgtgc 2315

aagtgtactt ttaaggccat cgtttgtacc cagagtcggc atggccacct aagtcttcat 2375

ttaatttatt gtccccaga aaagattaag atgctacttg aaaagactgt gaagattttt 2435

tacattgccca gataaaaagt gttacttaac caacaaacaa atgtaagact acaaaatcgt 2495

0060131-100400

tcaagagcaa ttctaataata atttacatat gttcacgcaa aatatgctta ggctgtcaaa 2555

ttagcacaac aaagaatgtg tttcactatc ttttctaggc taatttgtct tgagctgttg 2615

tctatagagc agtttacaga cttgtgtctt gtatcatttt ccagtgccag ggttctgaaa 2675

ttcattcaga acctgttaga ttaaagctgc accctgtgat tatttgaaaa gaattagctt 2735

gagagtaatg tcactatatt tgagttctta gagaagtatg agtggaactt gagtacagtt 2795

gaattattaa atatgcaagt tagaaattaa gtctactgaa aaatttacat tttgagtcag 2855

gttttgtgtc agtacttttag cagtttttga gaatgtgttt gatatcacag tgtttgtaaa 2915

ttctatgaaa aatgcatttt ccaaacaact tatacatgct ttttatgact atgcctaatz 2975

taaagaaaat gtattacatt ctgtatgtac aaagattaaa aatcaacctc ttttttgtgc 3035

tttaaaatga ctttgggatt aaaaaagcat atttcccaat cattgtcttc attccactac 3095

aaagtcacct cacagcatct tgctccactc ggcattctctg tgaaagcaac atgaaatgaa 3155

ctgtagtagg tgtgtagttt ggggaagtca aatggccatt ttatgtatgt gcatttggtg 3215

tcattggccg tggaacagaa tatatgttgg acctctgaaa agttgtaagg ggccaaatct 3275

aagtattctt cacggcagcc agaagttaac ggtggttagc gctgaggtat ggttgttgga 3335

cgaggccgat tttttttttt taacatggaa caatgaaacc aacaacaaac atttttaaaa 3395

ttaaaatgga taatttgtaa atagttttta gcttttaaaa tttaaagtgt ttttgagtgt 3455

gaaaagttga gtaaaactat ttgcaactgg ttttcagaaa agagaaaaga aacaacaaag 3515

gaattgaaac aggcagggag atcttaatac ctaatttcat catttctgca aaatgtactg 3575

ttttagaatg tattacaata tcaatgtgaa tatcttgaat cctgttataa atcctgcact 3635

gtattaaaca tgtaaatata ttgtttgtct gattagccaa tctcaccacc caaatgggga 3695

ggtatacatg tttgaagaac gtgtaactcg gtaattgatt tgttctgatg ttgtaactca 3755

atagaagtgt tttggaagga agcatgggtg gtgagacagt gtctgttctt ttgtgccagc 3815

tctgtatgat gtttgtaaga ccatgtttgt aagacatgaa taaattgctg cttttgccca 3875

aaaaaaaa aaaaaa 3891

<210> 2  
<211> 425  
<212> PRT  
<213> Homo sapiens  
<223> product = Repro-PC-1.0

<400> 2

Met Ala Pro Ile Thr Thr Ser Arg Glu Glu Phe Asp Glu Ile Pro Thr  
1 5 10 15

Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu  
20 25 30

Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr  
35 40 45

Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro  
50 55 60

Glu Asn Leu Asn Ser Lys Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu  
65 70 75 80

Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu  
85 90 95

Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro  
100 105 110

Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu  
115 120 125

Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser  
130 135 140

Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser  
145 150 155 160

Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu  
165 170 175

Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro  
180 185 190

Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr  
195 200 205

Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr

001001-12100000

210

215

220

Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe  
225 230 235 240

Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu  
245 250 255

Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu  
260 265 270

Met Asn Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg  
275 280 285

Gly Glu Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu  
290 295 300

Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser  
305 310 315 320

Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys  
325 330 335

Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala  
340 345 350

Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu  
355 360 365

Asp Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg  
370 375 380

Asn Glu Val Ile Gly Gln Leu Val Leu Gly Ala Ala Ala Glu Gly Thr  
385 390 395 400

Gly Gly Glu His Trp Lys Glu Ile Cys Asp Tyr Pro Arg Arg Gln Ile  
405 410 415

Ala Lys Trp His Val Leu Cys Asp Gly  
420 425

&lt;210&gt; 3

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

0010007 12100000

<220>  
<221> misc\_feature  
<222> (1)..(21)  
<223> 5' oligo (109) Upper Primer

<400> 3  
cagttttccc ttcagcacct c

21

<210> 4  
<211> 30  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(30)  
<223> 3' oligo (3489) Lower Primer

<400> 4  
ttcctttggt gtttcttttc tcttttctga

30

<210> 5  
<211> 425  
<212> PRT  
<213> rat

<220>  
<223> residues 1-425 = rat synaptotagmin 4 (SYT4)

<400> 5  
Met Ala Pro Ile Thr Thr Ser Arg Val Glu Phe Asp Glu Ile Pro Thr  
1 5 10 15  
Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu  
20 25 30  
Phe Ala Trp Ile Cys Cys Gln Arg Arg Ser Ala Lys Ser Asn Lys Thr  
35 40 45  
Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro  
50 55 60  
Glu Asn Leu Ser Ser Lys Lys Lys Phe Gly Gly Asp Asp Lys Ser Glu  
65 70 75 80  
Ala Lys Arg Lys Ala Ala Leu Pro Asn Leu Ser Leu His Leu Asp Leu



00400T "T2108360

85										90					95				
Glu	Lys	Arg	Asp	Leu	Asn	Gly	Asn	Phe	Pro	Lys	Thr	Asn	Pro	Lys	Ala				
			100					105					110						
Gly	Ser	Ser	Ser	Asp	Leu	Glu	Asn	Val	Thr	Pro	Lys	Leu	Phe	Pro	Glu				
			115				120					125							
Thr	Glu	Lys	Glu	Ala	Val	Ser	Pro	Glu	Ser	Leu	Lys	Ser	Ser	Thr	Ser				
	130					135					140								
Leu	Thr	Ser	Glu	Glu	Lys	Gln	Glu	Lys	Leu	Gly	Thr	Leu	Phe	Leu	Ser				
145					150					155					160				
Leu	Glu	Tyr	Asn	Phe	Glu	Lys	Lys	Ala	Phe	Val	Val	Asn	Ile	Lys	Glu				
				165					170					175					
Ala	Gln	Gly	Leu	Pro	Ala	Met	Asp	Glu	Gln	Ser	Met	Thr	Ser	Asp	Pro				
			180					185					190						
Tyr	Ile	Lys	Met	Thr	Ile	Leu	Pro	Glu	Lys	Lys	His	Lys	Val	Lys	Thr				
	195						200					205							
Arg	Val	Leu	Arg	Lys	Thr	Leu	Asp	Pro	Val	Phe	Asp	Glu	Thr	Phe	Thr				
	210					215					220								
Phe	Tyr	Gly	Val	Pro	Tyr	Pro	His	Ile	Gln	Glu	Leu	Ser	Leu	His	Phe				
225					230					235					240				
Thr	Val	Leu	Ser	Phe	Asp	Arg	Phe	Ser	Arg	Asp	Asp	Val	Ile	Gly	Glu				
				245					250					255					
Val	Leu	Val	Pro	Leu	Ser	Gly	Ile	Glu	Leu	Ser	Asp	Gly	Lys	Met	Leu				
			260					265					270						
Met	Thr	Arg	Glu	Ile	Ile	Lys	Arg	Asn	Ala	Lys	Lys	Ser	Ser	Gly	Arg				
	275						280					285							
Gly	Glu	Leu	Leu	Val	Ser	Leu	Cys	Tyr	Gln	Ser	Thr	Thr	Asn	Thr	Leu				
	290					295					300								
Thr	Val	Val	Val	Leu	Lys	Ala	Arg	His	Leu	Pro	Lys	Ser	Asp	Val	Ser				
305				310						315					320				
Gly	Leu	Ser	Asp	Pro	Tyr	Val	Lys	Val	Asn	Leu	Tyr	His	Ala	Lys	Lys				
				325					330					335					
Arg	Ile	Ser	Lys	Lys	Lys	Thr	His	Val	Lys	Lys	Cys	Thr	Pro	Asn	Ala				

001001 " F 2702950

340 345 350  
Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Ser Leu Glu  
355 360 365  
Glu Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg  
370 375 380  
Asn Glu Val Ile Gly Arg Leu Val Leu Gly Ala Thr Ala Glu Gly Ser  
385 390 395 400  
Gly Gly Gly His Trp Lys Glu Ile Cys Asp Phe Pro Arg Arg Gln Ile  
405 410 415  
Ala Lys Trp His Met Leu Cys Asp Gly  
420 425  
<210> 6  
<211> 117  
<212> PRT  
<213> Homo sapiens  
<220>  
<221> PEPTIDE  
<222> (1)..(117)  
<223> PKC-C2 internal repeat (amino acid positions  
154-271)  
<400> 6  
Glu Asn Val Pro Ser Leu Cys Gly Cys Asp His Thr Glu Arg Arg Gly  
1 5 10 15  
Arg Ile Tyr Leu Glu Ile Asn Val Lys Glu Asn Leu Leu Thr Val Gln  
20 25 30  
Ile Lys Glu Gly Arg Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser  
35 40 45  
Asp Pro Tyr Val Lys Val Lys Leu Ile Pro Asp Asp Lys Asp Gln Ser  
50 55 60  
Lys Lys Lys Thr Arg Thr Thr Lys Ala Cys Leu Asn Pro Val Trp Asn  
65 70 75 80  
Glu Thr Leu Thr Tyr Asp Leu Lys Pro Glu Asp Lys Asp Arg Arg Ile  
85 90 95

Leu Ile Glu Val Trp Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe Met  
100 105 110

Gly Ala Leu Ser Phe  
115

<210> 7

<211> 121

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(121)

<223> Repro-PC-1.0 (PC-20) "B" internal repeat (amino  
acid) positions 276-397

<400> 7

Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu  
1 5 10 15

Leu Ile Ser Leu Cys Tyr Gln Ser Thr Ile Asn Thr Leu Thr Val Val  
20 25 30

Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser  
35 40 45

Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser  
50 55 60

Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn  
65 70 75 80

Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser  
85 90 95

Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val  
100 105 110

Ile Gly Gln Leu Val Leu Gly Ala Ala  
115 120

<210> 8

<211> 115

<212> PRT

<213> rat

001001 "T" 000000

<220>

<221> PEPTIDE

<222> (1)..(115)

<223> synaptotagmin "B" internal repeat (amino acid  
positions 268-383)

<400> 8

Lys Glu Glu Gln Glu Lys Leu Gly Asp Ile Cys Phe Ser Leu Arg Tyr  
1 5 10 15

Val Pro Thr Ala Gly Lys Leu Thr Val Val Ile Leu Glu Ala Lys Asn  
20 25 30

Leu Lys Lys Met Asp Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile  
35 40 45

His Leu Met Gln Asn Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile  
50 55 60

Lys Lys Asn Thr Leu Asn Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu  
65 70 75 80

Val Pro Phe Glu Gln Ile Gln Lys Val Gln Val Val Val Thr Val Leu  
85 90 95

Asp Tyr Asp Lys Ile Gly Lys Asn Asp Ala Ile Gly Lys Val Phe Val  
100 105 110

Gly Tyr Asn  
115

<210> 9

<211> 120

<212> PRT

<213> rat

<220>

<221> PEPTIDE

<222> (1)..(120)

<223> synaptotagmin "A" internal repeat (amino acid  
positions 134-254)

<400> 9

Lys Glu Glu Pro Lys Glu Glu Glu Lys Leu Gly Lys Leu Gln Tyr Ser  
1 5 10 15

001001 "T41000000

Thr	Leu	Asp	Pro	Ala	Phe	Asp	Glu	Thr	Phe	Thr	Phe	Tyr	Gly	Ile	Pro
65					70					75					80

[illegible]











<400> 23

Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu Gly  
1 5 10 15

Glu Lys Glu Ser Val Ser Pro Glu Ser  
20 25

<210> 24

<211> 60

<212> PRT

<213> Homo sapiens

<400> 24

Leu Pro Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr  
1 5 10 15

Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr  
20 25 30

Thr Gln Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp  
35 40 45

Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu  
50 55 60

<210> 25

<211> 46

<212> PRT

<213> Homo sapiens

<400> 25

Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu Met Asn  
1 5 10 15

Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg Gly Glu  
20 25 30

Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu  
35 40 45

<210> 26

<211> 32

<212> PRT

<213> Homo sapiens

004001 "T 03362

<400> 26

Val Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu  
1 5 10 15

Val Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu  
20 25 30

<210> 27

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> residue 5=Val or Ile

<400> 27

Ser Asp Pro Tyr Xaa Lys  
1 5

001001 1111000000